

1 Table S1. Viral nucleotide substitution rate estimates

Viral group	Viral family	Viral genus	Common name	Rate estimate value (s/n/y)	Time-scale (year)	Alignment	Rate estimation method	Ref	Sampling count
<b>Short-term rate estimates</b>									
Group I/dsDNA virus	Adenoviridae	Mastadenovirus	Human adenovirus B	7.20E-5	24	Hexon coding region	Tip-date calibration under the Bayesian phylogenetic framework	(1)	1000
Group I/dsDNA virus	Adenoviridae	Mastadenovirus	Human adenovirus C	3.46E-5	21	Hexon coding region	Tip-date calibration under the Bayesian phylogenetic framework	(1)	1000
Group I/dsDNA virus	Herpesviridae	Simplexvirus	Human simplex virus 1 (nested in alpha herpesvirus, and alpha and beta herpesvirus)	8.21E-5	27	Thymidine kinase coding region	Tip-date calibration under the Bayesian phylogenetic framework	(1)	155
Group I/dsDNA virus	Herpesviridae	Varicellovirus	Varicella zoster virus (nested in alpha herpesvirus, and alpha and beta herpesvirus)	6.26E-6	37	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(1)	335
Group I/dsDNA virus	Papillomaviridae	Alphapapillomavirus	Human papillomavirus 16 (nested in papillomavirus)	3.94E-3	3	L1 protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(1)	510
Group I/dsDNA virus	Polyomaviridae	Orthopolyomavirus	Human polyomavirus JC	1.70E-5	33	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(2)	472
Group I/dsDNA virus	Polyomaviridae	Polyomavirus	BK virus	4.34E-5	29	Genome (coding region)	Tip-date calibration under the Bayesian phylogenetic framework	(1)	1000
Group I/dsDNA virus	Poxviridae	Orthopoxvirus	Variola virus	9.32E-6	36	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(1)	330
Group I/dsDNA virus	Poxviridae	Orthopoxvirus	Variola virus	1.7E-6	400	102 conserved genes	Internal-node calibration under the maximum-likelihood phylogenetic framework	(3)	350
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2	1.44E-3	27	Coat protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(4)	100
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2	1.21E-3	27	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(4)	97
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2	1.32E-3	27	ORF3	Tip-date calibration under the Bayesian phylogenetic framework	(4)	104
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2	1.03E-3	27	Replicase coding region	Tip-date calibration under the Bayesian phylogenetic framework	(4)	108
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2	8.74E-4	27	Replicase coding region-ORF3	Tip-date calibration under the Bayesian phylogenetic framework	(4)	92
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2a (nested in porcine circovirus 2)	1.64E-3	25	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(4)	499
Group II/ssDNA virus	Circoviridae	Circovirus	Porcine circovirus 2b (nested in porcine circovirus 2)	1.15E-3	9	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(4)	499
Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	3.45E-4	5	BC1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(5)	80

Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	1.37E-3	7	Coat protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(5)	56
Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	1.60E-3	7	DNA-A segment	Tip-date calibration under the Bayesian phylogenetic framework	(5)	67
Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	1.33E-4	5	DNA-B segment	Tip-date calibration under the Bayesian phylogenetic framework	(5)	64
Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	2.77E-4	5	Nuclear shuttle protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(5)	72
Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	1.24E-3	5	Replication-associated protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(5)	83
Group II/ssDNA virus	Geminiviridae	Begomovirus	African cassava mosaic disease-causing virus (nested in South American begomovirus)	1.56E-3	7	Ori-C1-C4	Tip-date calibration under the Bayesian phylogenetic framework	(6)	82
Group II/ssDNA virus	Geminiviridae	Begomovirus	Tomato yellow leaf curl virus (nested in South American begomovirus)	4.04E-4	18	Ori-C1-C4	Tip-date calibration under the Bayesian phylogenetic framework	(6)	89
Group II/ssDNA virus	Geminiviridae	Begomovirus	Tomato yellow leaf curl virus (nested in South American begomovirus)	4.63E-4	18	Coat protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(7)	113
Group II/ssDNA virus	Geminiviridae	Begomovirus	Tomato yellow leaf curl virus (nested in South American begomovirus)	2.88E-4	18	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(7)	90
Group II/ssDNA virus	Geminiviridae	Begomovirus	Tomato yellow leaf curl virus (nested in South American begomovirus)	1.37E-3	11	Intergenic region	Tip-date calibration under the Bayesian phylogenetic framework	(7)	105
Group II/ssDNA virus	Geminiviridae	Begomovirus	Tomato yellow leaf curl virus (nested in South American begomovirus)	1.75E-3	12	Intergenic region	Tip-date calibration under the Bayesian phylogenetic framework	(7)	107
Group II/ssDNA virus	Geminiviridae	Mastrevirus	Maize streak virus	3.87E-4	29	Ori-C1-C4	Tip-date calibration under the Bayesian phylogenetic framework	(6)	320
Group II/ssDNA virus	Geminiviridae	Mastrevirus	Maize streak virus	2.0E-4	6	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(8)	381
Group II/ssDNA virus	Geminiviridae	Mastrevirus	Maize streak virus	2.1E-4	6	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(8)	299
Group II/ssDNA virus	Geminiviridae	Mastrevirus	Sugarcane streak Reunion virus	1.82E-3	21	Ori-C1-C4	Tip-date calibration under the Bayesian phylogenetic framework	(6)	485
Group II/ssDNA virus	Geminiviridae	Mastrevirus	Sugarcane streak Reunion virus	3.5E-4	32	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(8)	515
Group II/ssDNA virus	Nanoviridae	Babuvirus	Banana bunchy top virus	1.43E-4	16	Genome	Internal-node calibration under the Bayesian phylogenetic framework	(9)	1000

Group II/ssDNA virus	Parvoviridae	Brevidensovirus	Infectious hypodermal and hematopoietic necrosis virus	1.39E-4	21	Capsid protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(10)	1000
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	1.83E-4	28	Coding region	Tip-date calibration under the Bayesian phylogenetic framework	(11)	82
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	1.72E-4	28	Coding region with unique gene rate; NS1	Tip-date calibration under the Bayesian phylogenetic framework	(11)	72
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	1.74E-4	28	Coding region with unique gene rate; NS1	Tip-date calibration under the Bayesian phylogenetic framework	(11)	83
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	2.07E-4	28	Coding region with unique gene rate; VP1	Tip-date calibration under the Bayesian phylogenetic framework	(11)	84
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	2.04E-4	28	Coding region with unique gene rate; VP1	Tip-date calibration under the Bayesian phylogenetic framework	(11)	84
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	1.90E-4	28	NS1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(11)	87
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	1.14E-4	28	VP1	Tip-date calibration under the Bayesian phylogenetic framework	(11)	92
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	2.60E-4	28	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(11)	66
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	1.20E-4	14	NS1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(12)	81
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	2.00E-4	14	NS1-VP1	Tip-date calibration under the Bayesian phylogenetic framework	(12)	84
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	2.30E-4	14	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(12)	88
Group II/ssDNA virus	Parvoviridae	Erythroparvovirus	Human B19	3.64E-4	34	ORF2	Tip-date calibration under the Bayesian phylogenetic framework	(13)	97
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Canine parvovirus	7.9E-5	26	NS1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(14)	323
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Canine parvovirus	1.7E-4	24	VP2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(14)	366
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Canine parvovirus	1.7E-4	26	VP2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(14)	311
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Feline panleukopenia parvovirus	7.9E-5	28	NS1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(14)	469
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Feline panleukopenia parvovirus	9.4E-5	34	VP2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(14)	531
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Porcine parvovirus	5.39E-5	33	NS1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(15)	512
Group II/ssDNA virus	Parvoviridae	Protoparvovirus	Porcine parvovirus	3.02E-4	33	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(15)	488
Group IV/(+)ssRNA virus	Arteriviridae	Arterivirus	Porcine reproductive and respiratory syndrome virus	3.29E-3	2	ORF5	Tip-date calibration under the Bayesian phylogenetic framework	(16)	495

Group IV/(+)ssRNA virus	Arteriviridae	Arterivirus	Porcine reproductive and respiratory syndrome virus	1.8E-3	3	ORF3,4, and 5	Tip-date calibration under the maximum-likelihood phylogenetic framework	(17)	505
Group IV/(+)ssRNA virus	Astroviridae	Mamastrovirus	Human astrovirus	1.03E-2	18	Outer-structural protein coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(18)	1000
Group IV/(+)ssRNA virus	Caliciviridae	Lagovirus	Rabbit hemorrhagic disease virus	7.70E-04	53	Capsid protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(19)	1000
Group IV/(+)ssRNA virus	Caliciviridae	Norovirus	Norwalk virus	4.97E-3 (4.30E-3, 5.60E-3, 5.10E-3)	34	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(20)	484
Group IV/(+)ssRNA virus	Caliciviridae	Norovirus	Norwalk virus	5.63E-3 (4.16E-3, 7.39E-3, 5.80E-3)	31	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(21)	516
Group IV/(+)ssRNA virus	Coronaviridae	Alphacoronavirus	Human coronavirus 229E	3.85E-4 (3.28E-4, 6.17E-4, 2.82E-4)	33	S protein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(22)	1000
Group IV/(+)ssRNA virus	Coronaviridae	Betacoronavirus	Bovine coronavirus	4.64E-4 (5.0E-4, 4.3E-4)	33	Spike protein coding region	Linear regression of the maximum-likelihood nucleotide substitution estimates against the years of isolation/ Tip-date calibration under the maximum-likelihood phylogenetic framework	(23)	1000
Group IV/(+)ssRNA virus	Coronaviridae	Betacoronavirus	SARS coronavirus	2.79E-3	2	ORF1	Tip-date calibration under the Bayesian phylogenetic framework	(24)	496
Group IV/(+)ssRNA virus	Coronaviridae	Betacoronavirus	SARS coronavirus	2.82E-3	4	ORF1	Tip-date calibration under the Bayesian phylogenetic framework	(25)	504
Group IV/(+)ssRNA virus	Coronaviridae	Gammacoronavirus	Avian coronavirus	9.40E-3	13	S1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(26)	336
Group IV/(+)ssRNA virus	Coronaviridae	Gammacoronavirus	Avian coronavirus	1.70E-3	25	S1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(26)	323
Group IV/(+)ssRNA virus	Coronaviridae	Gammacoronavirus	Avian coronavirus	2.40E-3	41	S1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(26)	341
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 1 virus	4.55E-4	54	E coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(27)	499
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 1 virus	6.50E-4	43	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(28)	501
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 2 virus	6.07E-4	54	E coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(27)	235
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 2 virus	5.66E-4	19	E coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(29)	250
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 2 virus	6.50E-4	51	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(30)	250
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 2 virus	8.0E-4	21	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(31)	265
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 3 virus	9.01E-4	44	E coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(27)	252
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 3 virus	1.03E-3	18	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(32)	244

Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 3 virus	8.48E-4	7	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(33)	252
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 3 virus	8.9E-4	50	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(34)	252
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 4 virus	6.02E-4	38	E coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(27)	338
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 4 virus	8.3E-4	18	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(31)	353
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Dengue 4 virus	1.07E-3	26	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(35)	309
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Japanese encephalitis virus	4.35E-04	74	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(36)	1000
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Kyasanur forest disease virus	6.4E-4	49	Envelop-NS5	Tip-date calibration under the Bayesian phylogenetic framework	(37)	1000
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	St. Louis encephalitis virus	2.17E-4	78	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(38)	503
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	St. Louis encephalitis virus	4.1E-4	72	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(39)	497
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	West Nile virus	8.5E-4	8	E coding region	Tip-date calibration under the Bayesian phylogenetic framework	(40)	1000
Group IV/(+)ssRNA virus	Flaviviridae	Flavivirus	Yellow fever virus	4.2E-4	76	prM/E	Tip-date calibration under the Bayesian phylogenetic framework	(41)	1000
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	2.1E-3	17	E2-P7-NS2	Tip-date calibration under the Bayesian phylogenetic framework	(42)	100
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.3E-3	30	E2-P7-NS2	Tip-date calibration under the Bayesian phylogenetic framework	(42)	118
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.2E-3	17	NSSB coding region	Tip-date calibration under the Bayesian phylogenetic framework	(42)	111
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.0E-3	30	NSSB coding region	Tip-date calibration under the Bayesian phylogenetic framework	(42)	107
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.9E-3	17	NSSB coding region with E2-P7-NS2 rate prior	Tip-date calibration under the Bayesian phylogenetic framework	(42)	105
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.0E-3	30	NSSB with E2-P7-NS2 rate prior	Tip-date calibration under the Bayesian phylogenetic framework	(42)	134
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.12E-3 (1.12E-3, 1.11E-3, 1.13E-3, 1.11E-3)	19	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(43)	127
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.17E-3 (1.04E-3, 1.25E-3, 1.24E-3, 1.18E-3)	19	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(43)	97
Group IV/(+)ssRNA virus	Flaviviridae	Hepacivirus	Hepatitis C virus	1.42E-3 (1.30E-3, 1.44E-3, 1.47E-3, 1.48E-3)	19	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(43)	101

Group IV/(+)ssRNA virus	Flaviviridae	Pegivirus	GB virus C	3.42E-3 (4.13E-3, 4.15E-3, 2.10E-3, 4.45E-3, 4.13E-3, 2.09E-3, 5.03E-3, 4.99E-3, 1.85E-3)	9	5'UTR	Tip-date calibration under the Bayesian phylogenetic framework	(44)	267
Group IV/(+)ssRNA virus	Flaviviridae	Pegivirus	GB virus C	3.50E-2 (5.43E-2, 4.33E-2, 3.28E-2, 1.94E-2, 3.95E-2, 3.95E-2, 2.49E-2, 4.30E-2, 3.16E-2)	4	E1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(44)	243
Group IV/(+)ssRNA virus	Flaviviridae	Pegivirus	GB virus C	9.33E-3 (2.19E-2, 1.46E-2, 3.53E-3, 2.74E-2, 7.92E-3, 2.61E-3, 2.89E-2, 8.67E-3, 3.34E-3)	3	E2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(44)	260
Group IV/(+)ssRNA virus	Flaviviridae	Pegivirus	GB virus C	1.65E-2 (3.55E-2, 2.12E-2, 1.52E-2, 3.58E-2, 8.49E-3, 6.99E-3, 3.24E-2, 1.14E-2, 1.02E-2)	4	NS5b coding region	Tip-date calibration under the Bayesian phylogenetic framework	(44)	230
Group IV/(+)ssRNA virus	Luteoviridae	Luteovirus	Barley yellow dwarf virus	1.5E-3	89	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	232
Group IV/(+)ssRNA virus	Luteoviridae	Luteovirus	Barley yellow dwarf virus	6.7E-3	89	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	262
Group IV/(+)ssRNA virus	Luteoviridae	Luteovirus	Barley yellow dwarf virus	6.0E-4	89	RTD	Tip-date calibration under the Bayesian phylogenetic framework	(45)	240
Group IV/(+)ssRNA virus	Luteoviridae	Luteovirus	Barley yellow dwarf virus	3.16E-4	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(46)	266
Group IV/(+)ssRNA virus	Luteoviridae	Luteovirus	Soybean dwarf virus	6.0E-4	17	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	514
Group IV/(+)ssRNA virus	Luteoviridae	Luteovirus	Soybean dwarf virus	2.3E-3	17	RTD	Tip-date calibration under the Bayesian phylogenetic framework	(45)	486
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Beet chlorosis virus	2.7E-3	20	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	334
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Beet chlorosis virus	7.2E-3	20	P0 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	332
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Beet chlorosis virus	1.6E-3	20	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	334
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Beet mild yellowing virus	7.7E-4	25	P0 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	508
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Beet mild yellowing virus	3.7E-4	25	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	492
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Cereal yellow dwarf virus-RPV	7.4E-4	81	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	363
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Cereal yellow dwarf virus-RPV	2.3E-2	81	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	316

Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Cereal yellow dwarf virus-RPV	3.3E-3	81	RTD	Tip-date calibration under the Bayesian phylogenetic framework	(45)	321
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Cucurbit aphid-borne yellows virus	3.5E-2	5	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	503
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Cucurbit aphid-borne yellows virus	4.3E-3	5	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	497
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Potato leafroll virus	6.2E-4	34	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	488
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Potato leafroll virus	3.4E-4	34	P0 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	512
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Sugarcane yellow leaf virus	1.1E-3	19	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	311
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Sugarcane yellow leaf virus	1.2E-3	19	P0 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	351
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Sugarcane yellow leaf virus	1.4E-4	19	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	338
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Turnip yellows virus	8.6E-4	26	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	317
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Turnip yellows virus	2.7E-3	26	P0 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	350
Group IV/(+)ssRNA virus	Luteoviridae	Polerovirus	Turnip yellows virus	1.0E-3	26	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(45)	333
Group IV/(+)ssRNA virus	Picornaviridae	Aphthovirus	Foot-and-mouth disease virus	1.45E-3	38	3DPol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	341
Group IV/(+)ssRNA virus	Picornaviridae	Aphthovirus	Foot-and-mouth disease virus	1.46E-3	75	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(48)	321
Group IV/(+)ssRNA virus	Picornaviridae	Aphthovirus	Foot-and-mouth disease virus	2.26E-5	0.58	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(49)	338
Group IV/(+)ssRNA virus	Picornaviridae	Cardiovirus	Encephalomyocarditis virus	1.61E-3	22	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	1000
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus A	5.53E-3	24	3DPol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	252
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus A	3.66E-3	29	1D coding region	Tip-date calibration under the Bayesian phylogenetic framework	(50)	246
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus A	3.19E-3	40	3CD coding region	Tip-date calibration under the Bayesian phylogenetic framework	(50)	261
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus A	8.65E-3	59	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(51)	241
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus B	5.73E-3	48	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	194
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus B	5.27E-3	62	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	223
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus B	4.2E-3	26	VP1-P1	Tip-date calibration under the Bayesian phylogenetic framework	(52)	180
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus B	8.8E-3	9	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(53)	193

Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus B	8.5E-3	49	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(53)	210
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus C	11.68E-3	24	3DPol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	521
Group IV/(+)ssRNA virus	Picornaviridae	Enterovirus	Enterovirus C	9E-3	10	VP1-2A	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(54)	479
Group IV/(+)ssRNA virus	Picornaviridae	Hepadovirus	Hepatitis A virus	8.9E-4	32	3DPol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	182
Group IV/(+)ssRNA virus	Picornaviridae	Hepadovirus	Hepatitis A virus	1.73E-4	33	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(55)	219
Group IV/(+)ssRNA virus	Picornaviridae	Hepadovirus	Hepatitis A virus	1.99E-4	33	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(55)	206
Group IV/(+)ssRNA virus	Picornaviridae	Hepadovirus	Hepatitis A virus	2.38E-4	17	VP1 (3 <sup>rd</sup> codon)	Tip-date calibration under the Bayesian phylogenetic framework	(56)	204
Group IV/(+)ssRNA virus	Picornaviridae	Hepadovirus	Hepatitis A virus	9.76E-4	17	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(56)	189
Group IV/(+)ssRNA virus	Picornaviridae	Parechovirus	Human parechovirus	2.96E-3	34	3DPol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	311
Group IV/(+)ssRNA virus	Picornaviridae	Parechovirus	Human parechovirus	2.21E-3	51	P1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(57)	352
Group IV/(+)ssRNA virus	Picornaviridae	Parechovirus	Human parechovirus	2.79E-3	32	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(57)	337
Group IV/(+)ssRNA virus	Picornaviridae	Teschovirus	Porcine teschovirus	1.62E-3	50	VP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(47)	1000
Group IV/(+)ssRNA virus	Potyviridae	Potyvirus	American cowpea aphid-borne mosaic virus	1.397E-4	500	cCP coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred from human migration history	(58)	1000
Group IV/(+)ssRNA virus	Potyviridae	Potyvirus	American papaya ringspot virus	1.25E-4	300	cCP coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred from human migration history	(58)	1000
Group IV/(+)ssRNA virus	Potyviridae	Potyvirus	Australian potyvirus	1.173E-4	75	cCP coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred from human migration history	(58)	1000
Group IV/(+)ssRNA virus	Potyviridae	Potyvirus	Plum poxvirus	1.40E-4	100	cCP coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred from the date of the Plum pox disease outbreak in Bulgaria	(58)	1000
Group IV/(+)ssRNA virus	Potyviridae	Potyvirus	Zucchini yellow mosaic virus	5.0E-4	22	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(59)	1000
Group IV/(+)ssRNA virus	Togaviridae	Alphavirus	Fort Morgan virus	1.81E-4	9	Capsid-E3-E2-6K-E1	Tip-date calibration under the Bayesian phylogenetic framework	(60)	499

Group IV/(+)ssRNA virus	Togaviridae	Alphavirus	Fort Morgan virus	2.64E-4	32	Capsid-E3-E2-6K-E1	Tip-date calibration under the Bayesian phylogenetic framework	(60)	501
Group IV/(+)ssRNA virus	Togaviridae	Alphavirus	Ross River virus	7.53E-4 (8.13E-4, 8.55E-4, 6.91E-4, 7.45E-4, 6.78E-4)	45	E2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(61)	1000
Group IV/(+)ssRNA virus	Togaviridae	Alphavirus	Venezuelan equine encephalitis virus	1.28E-4	54	Structural polyprotein coding region	Tip-date calibration under the Bayesian phylogenetic framework	(62)	1000
Group IV/(+)ssRNA virus	Unclassified	Sobemovirus	Rice Yellow Mottle Virus	11.7E-4	40	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(63)	346
Group IV/(+)ssRNA virus	Unclassified	Sobemovirus	Rice Yellow Mottle Virus	7.3E-4	40	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(64)	325
Group IV/(+)ssRNA virus	Unclassified	Sobemovirus	Rice Yellow Mottle Virus	7.7E-4	40	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(64)	329
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Cucumber green mottle mosaic virus (nested in tobamovirus)	8.0E-4	38	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Cucumber green mottle mosaic virus (nested in tobamovirus)	6.7E-4	38	MP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Cucumber green mottle mosaic virus (nested in tobamovirus)	8.0E-5	38	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Odontoglossum ringspot virus (nested in tobamovirus)	7.8E-4	44	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Odontoglossum ringspot virus (nested in tobamovirus)	1.3E-3	44	MP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Odontoglossum ringspot virus (nested in tobamovirus)	7.7E-4	44	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Odontoglossum ringspot virus (nested in tobamovirus)	8.8E-4	44	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Pepper mild mottle virus (nested in tobamovirus)	1.8E-4	36	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Pepper mild mottle virus (nested in tobamovirus)	8.9E-4	36	MP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Pepper mild mottle virus (nested in tobamovirus)	2.6E-4	36	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Pepper mild mottle virus (nested in tobamovirus)	2.6E-4	36	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobacco mild green mosaic virus (nested in tobamovirus)	1.7E-4	101	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobacco mild green mosaic virus (nested in tobamovirus)	1.3E-4	101	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobacco mild green mosaic virus (nested in tobamovirus)	1.4E-4	101	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobacco mosaic virus (nested in tobamovirus)	1.6E-4	109	CP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobacco mosaic virus (nested in tobamovirus)	2.9E-4	109	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*

Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobacco mosaic virus (nested in tobamovirus)	7.9E-4	109	RdRp coding region	Tip-date calibration under the Bayesian phylogenetic framework	(65)	0*
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Araraquara hantavirus (nested in rodent hantavirus)	5.11E-3 (8.65E-3, 9.05E-3, 1.08E-2, 2.68E-3, 2.62E-3, 3.01E-3)	6	G1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(66)	248
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Araraquara hantavirus (nested in rodent hantavirus)	3.34E-3 (2.67E-3, 2.52E-3, 6.26E-3, 3.01E-3, 2.98E-3, 3.69E-3)	6	G2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(66)	247
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Araraquara hantavirus (nested in rodent hantavirus)	2.67E-3 (2.49E-3, 2.43E-3 3.23E-3, 2.48E-3, 2.63E-3, 2.84E-3)	6	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(66)	246
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Dobrava hantavirus (nested in rodent hantavirus)	3.23E-4 (2.99E-4, 2.80E-4, 4.74E-4, 2.66E-4, 2.90E-4, 3.74E-4)	21	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(66)	741
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Puumala hantavirus (nested in Puumala and Tula hantavirus, and rodent hantavirus)	5.75E-4 (6.09E-4, 5.41E-4, 6.22E-4, 5.20E-4, 5.51E-4, 6.14E-4)	25	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(66)	0*
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Rodent hantavirus	6.76E-4	28	S segment	Tip-date calibration under the Bayesian phylogenetic framework	(67)	0*
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Sin Nombre virus (nested in rodent hantavirus)	6.76E-3	12	M segment	Tip-date calibration under the Bayesian phylogenetic framework	(68)	362
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Sin Nombre virus (nested in rodent hantavirus)	1.93E-3	12	S segment	Tip-date calibration under the Bayesian phylogenetic framework	(68)	379
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Tula hantavirus (nested in Puumala and Tula hantavirus, and rodent hantavirus)	1.25E-2 (1.99E-2, 2.10E-2, 1.84E-2, 8.07E-3, 6.77E-3, 8.87E-3)	9	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(66)	252
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	1.01E-4	47	L segment	Tip-date calibration under the maximum-likelihood phylogenetic framework	(69)	123
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	1.02E-4	47	L segment	Tip-date calibration under the maximum-likelihood phylogenetic framework	(69)	96
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	0.92E-4	47	M segment	Tip-date calibration under the maximum-likelihood phylogenetic framework	(69)	118
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	1.22E-4	47	M segment	Tip-date calibration under the maximum-likelihood phylogenetic framework	(69)	99
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	0.27E-4	47	S segment	Tip-date calibration under the maximum-likelihood phylogenetic framework	(69)	105
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	0.34E-4	47	S segment	Tip-date calibration under the maximum-likelihood phylogenetic framework	(69)	111
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	5.8E-5	47	L segment	Tip-date calibration under the Bayesian phylogenetic framework	(70)	114

Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	1.52E-4	47	M segment	Tip-date calibration under the Bayesian phylogenetic framework	(70)	124
Group V/(-)ssRNA virus	Bunyaviridae	Nairovirus	Crimean-Congo hemorrhagic fever virus	1.09E-4	49	S segment	Tip-date calibration under the Bayesian phylogenetic framework	(70)	110
Group V/(-)ssRNA virus	Bunyaviridae	Phlebovirus	Rift valley fever virus	2.78E-4	56	L segment	Tip-date calibration under the Bayesian phylogenetic framework	(71)	175
Group V/(-)ssRNA virus	Bunyaviridae	Phlebovirus	Rift valley fever virus	2.42E-4	56	M segment	Tip-date calibration under the Bayesian phylogenetic framework	(71)	166
Group V/(-)ssRNA virus	Bunyaviridae	Phlebovirus	Rift valley fever virus	2.35E-4	56	S segment	Tip-date calibration under the Bayesian phylogenetic framework	(71)	152
Group V/(-)ssRNA virus	Bunyaviridae	Phlebovirus	Rift valley fever virus	2.8E-4	0.5	L segment	Tip-date calibration under the Bayesian phylogenetic framework	(72)	167
Group V/(-)ssRNA virus	Bunyaviridae	Phlebovirus	Rift valley fever virus	3.6E-4	0.5	M segment	Tip-date calibration under the Bayesian phylogenetic framework	(72)	175
Group V/(-)ssRNA virus	Bunyaviridae	Phlebovirus	Rift valley fever virus	3.9E-4	0.5	S segment	Tip-date calibration under the Bayesian phylogenetic framework	(72)	165
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.67E-3	0.25	HA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	31
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.55E-3	0.25	MP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	35
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.65E-3	0.25	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	35
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.59E-3	0.25	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	29
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.62E-3	0.25	NS coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	24
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.45E-3	0.25	PA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	24
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.34E-3	0.25	PB1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	26
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.60E-3	0.25	PB2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(73)	30
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.92E-3	29	HA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	38
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.49E-3	32	MP1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	28
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.61E-3	48	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	42
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.17E-3	42	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	28
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.87E-3	42	NS1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	30
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.48E-3	49	PA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	26
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.86E-3	42	PB1 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	22

Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.15E-3	49	PB2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(74)	41
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	5.42E-4	37	M segment	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(75)	30
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	5.06E-4	37	NS segment	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(75)	33
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	7.84E-3	1	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(76)	30
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	4.31E-3	11	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(77)	21
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	1.82E-3	23	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(77)	19
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.12E-3	29	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(77)	29
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.11E-3	39	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(77)	32
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.20E-3	72	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(77)	20
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.28E-3	76	NA coding region	Tip-date calibration under the Bayesian phylogenetic framework	(77)	27
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.43E-3	1	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	31
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.8E-3	30	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	38
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	9E-4	45	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	27
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.25E-3	55	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	35
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.29E-3	79	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	15
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	3.41E-3	82	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	26
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	1.98E-3	91	NP coding region	Tip-date calibration under the Bayesian phylogenetic framework	(78)	28
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.28E-3	27	NA coding region	Linear regression of the maximum-likelihood nucleotide substitution estimates against the years of isolation	(79)	27
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus A	Influenza A virus	2.58E-3	27	NA coding region	Linear regression of the maximum-likelihood nucleotide substitution estimates against the years of isolation	(79)	43
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	1.39E-3	13	HA coding region	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	132

Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	2.41E-3	19	HA coding region	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	145
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	1.09E-3	19	M coding region	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	128
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	1.31E-3	9	M segment	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	147
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	0.95E-3	19	NP coding region	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	151
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	0.45E-3	14	NS coding region	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	158
Group V/(-)ssRNA virus	Orthomyxoviridae	Influenzavirus B	Influenza B virus	0.87E-3	21	NS coding region	Linear regression of neighbour-joining nucleotide substitution estimates against the years of isolation	(80)	139
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Avian metapneumovirus	1.39E-3	9	F coding region	Tip-date calibration under the Bayesian phylogenetic framework	(81)	234
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Avian metapneumovirus	6.14E-3	9	M2 coding region	Tip-date calibration under the Bayesian phylogenetic framework	(81)	258
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Avian metapneumovirus	4.47E-3	9	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(81)	259
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Avian metapneumovirus	7.01E-3	9	P coding region	Tip-date calibration under the Bayesian phylogenetic framework	(81)	249
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	4.58E-3	4	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(82)	149
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	7.87E-3	6	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(82)	156
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	6.14E-3	21	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(82)	127
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	6.48E-3	21	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(82)	137
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	5.18E-3	23	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(82)	145
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	5.34E-3	23	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(82)	140
Group V/(-)ssRNA virus	Paramyxoviridae	Metapneumovirus	Human metapneumovirus	7.12E-4	25	F coding region	Tip-date calibration under the Bayesian phylogenetic framework	(83)	146
Group V/(-)ssRNA virus	Paramyxoviridae	Morbillivirus	Canine distemper virus	1.17E-3	19	H coding region	Tip-date calibration under the Bayesian phylogenetic framework	(84)	1000
Group V/(-)ssRNA virus	Paramyxoviridae	Morbillivirus	Measles virus	6.58E-4	29	H coding region	Tip-date calibration under the Bayesian phylogenetic framework	(84)	186
Group V/(-)ssRNA virus	Paramyxoviridae	Morbillivirus	Measles virus	8.69E-4	26	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(84)	213

Group V/(-)ssRNA virus	Paramyxoviridae	Morbillivirus	Measles virus	3.4E-4	33	H coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(85)	178
Group V/(-)ssRNA virus	Paramyxoviridae	Morbillivirus	Measles virus	6.44E-4	55	H coding region	Tip-date calibration under the Bayesian phylogenetic framework	(86)	201
Group V/(-)ssRNA virus	Paramyxoviridae	Morbillivirus	Measles virus	6.02E-4	55	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(86)	222
Group V/(-)ssRNA virus	Paramyxoviridae	Pneumovirus	Human respiratory syncytial virus	1.83E-3	47	G coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(87)	349
Group V/(-)ssRNA virus	Paramyxoviridae	Pneumovirus	Human respiratory syncytial virus	1.95E-3	44	G coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(88)	329
Group V/(-)ssRNA virus	Paramyxoviridae	Pneumovirus	Human respiratory syncytial virus	2.5E-3	5	G coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(89)	322
Group V/(-)ssRNA virus	Paramyxoviridae	Pneumovirus	Respiratory syncytial virus	2.31E-3	10	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(90)	1000
Group V/(-)ssRNA virus	Paramyxoviridae	Rubulavirus	Mumps virus	9.17E-4	54	HN coding region	Tip-date calibration under the Bayesian phylogenetic framework	(84)	1000
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	5.10E-5	35	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(91)	76
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	6.11E-5	35	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(91)	48
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	2.32E-4	27	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(92)	54
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	1.53E-4	40	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(93)	66
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	1.68E-3	13	G-L intergenic region	Tip-date calibration under the Bayesian phylogenetic framework	(94)	62
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	8.26E-4	20	G-L intergenic region	Tip-date calibration under the Bayesian phylogenetic framework	(94)	66
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	3.57E-4	14	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(95)	53
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	2.75E-4	16	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(95)	62
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	2.57E-4	19	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(95)	58
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	3.90E-4	20	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(95)	75
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	3.32E-4	26	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(95)	61
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	2.59E-4	20	P coding region	Tip-date calibration under the Bayesian phylogenetic framework	(95)	64
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	2.7E-4	33	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(96)	68
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	3.9E-4	25	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(97)	69
Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	2.3E-4	36	N coding region	Tip-date calibration under the Bayesian phylogenetic framework	(97)	55

Group V/(-)ssRNA virus	Rhabdoviridae	Lyssavirus	Rabies virus	3.96E-4	39	G coding region	Tip-date calibration under the Bayesian phylogenetic framework	(98)	63
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 1	5.15E-6	760	Env coding region	Internal-node calibration under the maximum-likelihood phylogenetic framework	(99)	182
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 1	1.77E-6	760	LTR	Internal-node calibration under the maximum-likelihood phylogenetic framework	(99)	206
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 2	4.32E-5	62.5	LTR	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution	(100)	339
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 2	2.7E-4	14	LTR	Dividing the difference between neighbour-joining nucleotide substitution estimates by the difference between the years of isolation	(101, 102)	333
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	3.03E-3	1	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	27
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	2.48E-3	2	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	26
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	3.89E-3	3	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	28
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	3.47E-3	4	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	30
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	3.00E-3	5	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	28
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.08E-3	6	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	32
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.27E-3	7	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	20
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.19E-3	7	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	24
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.67E-3	8	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	33
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.32E-3 (1.14E-3, 1.54E-3)	4.1	Env coding region	Tip-date calibration under the Bayesian phylogenetic framework	(103)	23
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.66E-3	0.7	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	17
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.54E-3	0.8	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	28
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.06E-3	1.0	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	30
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	2.57E-3	1.3	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	32
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	2.30E-3	1.6	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	25

Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	3.88E-3	2.3	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	23
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.13E-3	2.5	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	31
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.65E-3	2.9	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	24
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.95E-3	4.1	Env coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	27
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	4.75E-3	1	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	33
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	6.21E-3	2	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	29
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	5.87E-3	3	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	19
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	2.83E-3	4	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	30
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.85E-3	5	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	31
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.22E-3	6	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	23
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.07E-3	7	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	23
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.38E-3	7	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	19
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.03E-3	8	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(103)	33
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.10E-3 (0.77E-3, 1.54E-3)	4.1	Pol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(103)	20
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	2.28E-3	0.7	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	21
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.46E-3	0.8	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	27
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.84E-3	1.0	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	28
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.52E-3	1.3	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	24
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.72E-3	1.6	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	29
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	2.35E-3	2.3	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	27
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	1.35E-3	2.5	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	23
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.50E-3	2.9	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	27
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Feline immunodeficiency virus	0.39E-3	4.1	Pol coding region	Tip-date calibration under the maximum-likelihood phylogenetic framework	(103)	26

Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	0.96E-3	14	Pol coding region	Dividing an average neighbour-joining nucleotide substitution estimates by the timescale of evolution	(104)	21
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.08E-2	7	Vpu coding region	Tip-date calibration under the Bayesian phylogenetic framework	(105)	16
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.13E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	11
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.42E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	14
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.55E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	14
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.55E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	10
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.89E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	16
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.41E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	26
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.46E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	14
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.55E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	17
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.56E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	19
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	3.63E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	16
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.74E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	18
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.41E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	24
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.25E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	26

Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.35E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	21
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.04E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	19
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.06E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	19
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.25E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	17
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	3.43E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	12
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.25E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	13
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.39E-3	2	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(106)	25
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.50E-3	11	Pol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(107)	15
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	1.80E-3	12	Pol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(107)	16
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	2.06E-3	15	Pol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(108)	21
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	3.15E-3	20	Pol coding region	Tip-date calibration under the Bayesian phylogenetic framework	(109)	15
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Human immunodeficiency virus (nested in simian immunodeficiency virus)	4.65E-3	14	Env coding region	Tip-date calibration under the Bayesian phylogenetic framework	(110)	15
Group VII/RT-DNA virus	Hepadnaviridae	Avihepadnavirus	Avian hepatitis B virus	7.32E-4	20	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(111)	38
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	7.72E-4	22	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(111)	93
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	3.39E-5 (2.60E-5, 4.43E-5)	21	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(112)	92
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	6.15E-5 (6.10E-5, 6.20E-5)	23	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(112)	102
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	8.1E-5	17	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	85

Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	1.2E-5	17.5	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	107
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	1.2E-5	18	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	99
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	2.1E-4	18	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	103
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	3.0E-5	18.6	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	86
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	8.6E-5	18.9	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	100
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	8.0E-6	20.1	Genome	Tip-date calibration under the Bayesian phylogenetic framework	(113)	95

**Long-term rate estimate**

Group I/dsDNA virus	Herpesviridae	Cytomegalovirus, Muromegalovirus, Varicellovirus	Alpha and beta herpesvirus	3E-9	112E6	UL2-UL5- UL15-UL19- UL27-UL28- UL29-UL30	Linear regression of maximum-likelihood nucleotide substitution estimates against viral divergence dates, inferred under the viral-host co-speciation assumption	(114)	345
Group I/dsDNA virus	Herpesviridae	Simplexvirus, Varicellovirus	Alpha herpesvirus (nested in alpha and beta herpesvirus)	2.7E-9	60E6	gB (excluding the 3 <sup>rd</sup> codon position)	Linear regression of maximum-likelihood nucleotide substitution estimates against viral divergence dates, inferred under the viral-host co-speciation assumption	(115)	320
Group I/dsDNA virus	Herpesviridae	Simplexvirus	Human simplex virus 1 (nested in alpha herpesvirus, and alpha and beta herpesvirus)	1.82E-8	8.45E6	US7-US8	Internal-node calibration under the Bayesian phylogenetic framework	(116)	180
Group I/dsDNA virus	Papillomaviridae	Alphapapillomavirus, Betapapillomavirus, Gammapapillomavirus, Deltapapillomavirus, Epsilonpapillomavirus, Mupapillomavirus, Nupapillomavirus, Pipapillomavirus, Kappapapillomavirus, Sigmapapillomavirus, Xipapillomavirus, Dyoxipapillomavirus, Omkronpapillomavirus, Upsilonpapillomavirus, Taupapillomavirus, Lambdapapillomavirus	Papillomavirus	7.1E-9	95.65E6	E1 coding region	Internal-node calibration under the Bayesian phylogenetic framework	(117)	235
Group I/dsDNA virus	Papillomaviridae	Alphapapillomavirus, Betapapillomavirus, Gammapapillomavirus, Deltapapillomavirus, Epsilonpapillomavirus, Mupapillomavirus,	Papillomavirus	9.6E-9	95.65E6	L1 coding region	Internal-node calibration under the Bayesian phylogenetic framework	(117)	255

		Nupapillomavirus, Pipapillomavirus, Kappapapillomavirus, Sigmapapillomavirus, Xipapillomavirus, Dyoxipapillomavirus, Omkronpapillomavirus, Upsilonpapillomavirus, Taupapillomavirus, Lambda papillomavirus						
Group I/dsDNA virus	Papillomaviridae	Dyozetapapillomavirus, Etapapillomavirus, Thetapapillomavirus	Avian and turtle papillomavirus (nested in papillomavirus)	1.1E-8	227.5E6	E1 coding region	Internal-node calibration under the Bayesian phylogenetic framework	(118) 136
Group I/dsDNA virus	Papillomaviridae	Dyozetapapillomavirus, Etapapillomavirus, Thetapapillomavirus	Avian and turtle papillomavirus (nested in papillomavirus)	1.2E-8	227.5E6	E2 coding region	Internal-node calibration under the Bayesian phylogenetic framework	(118) 123
Group I/dsDNA virus	Papillomaviridae	Dyozetapapillomavirus, Etapapillomavirus, Thetapapillomavirus	Avian and turtle papillomavirus (nested in papillomavirus)	0.9E-8	227.5E6	L1 coding region	Internal-node calibration under the Bayesian phylogenetic framework	(118) 135
Group I/dsDNA virus	Papillomaviridae	Dyozetapapillomavirus, Etapapillomavirus, Thetapapillomavirus	Avian and turtle papillomavirus (nested in papillomavirus)	2.2E-8	227.5E6	L2 coding region	Internal-node calibration under the Bayesian phylogenetic framework	(118) 116
Group I/dsDNA virus	Papillomaviridae	Lambda papillomavirus	Feline papillomavirus (nested in papillomavirus)	1.95E-8	10.78E6	E6-E7-E1-E2-L2-L1	Internal-node calibration under the Bayesian phylogenetic framework	(119) 510
Group I/dsDNA virus	Polyomaviridae	Orthopolyomavirus	Human polyomavirus JC	2E-7	1E5	IG coding region	Dividing an average neighbour-joining nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(120) 528
Group I/dsDNA virus	Poxviridae	Orthopoxvirus	Variola virus (Poxvirus)	5E-7	8600	35 conserved genes	Internal-node calibration under the maximum-likelihood phylogenetic framework	(121) 320
Group II/ssDNA virus	Geminiviridae	Begomovirus	South American begomovirus	5.79E-7	1.9E6	Coat protein coding region	Dividing an upper-bound maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(122) 496
Group II/ssDNA virus	Geminiviridae	Mastrevirus	Wheat dwarf virus	1.33E-8	12E6	Genome	Dividing a neighbour-joining nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(123) 1000
Group IV/(+)ssRNA virus	Virgaviridae	Tobamovirus	Tobamovirus	2.16E-8	100E6	Coat protein coding region	Internal-node calibration under the maximum-likelihood phylogenetic framework	(122) 1000
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Puumala and Tula hantavirus (nested in rodent hantavirus)	2.64E-7	4.75E6	S segment-N coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(124) 489

Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Puumala hantavirus (nested in Puumala and Tula hantavirus, and rodent hantavirus)	1.41E-7	2E6	S segment-N coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(124)	252
Group V/(-)ssRNA virus	Bunyaviridae	Hantavirus	Rodent hantavirus	1.04E-6	10E6	S segment-N coding region	Dividing an average maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(124)	259
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 1	1.54E-6	50000	LTR-Env	Internal-node calibration under the maximum-likelihood phylogenetic framework	(125)	205
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 1	2.1E-7	50000	Env coding region	Internal-node calibration under the Bayesian phylogenetic framework	(126)	190
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 1	5.6E-7	50000	LTR	Internal-node calibration under the Bayesian phylogenetic framework	(126)	217
Group VI/RT-RNA virus	Retroviridae	Deltaretrovirus	Human T-lymphotropic virus 2	1.02E-6	25000	LTR	Internal-node calibration under the maximum-likelihood phylogenetic framework	(101, 102)	328
Group VI/RT-RNA virus	Retroviridae	Lentivirus	Simian immunodeficiency virus	7.3E-6	10000	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(127)	530
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Ape foamy virus (nested in Old World monkey and ape foamy virus, simian foamy virus, and foamy virus)	1.41E-8	16.52E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	54
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Ape foamy virus (nested in Old World monkey and ape foamy virus, simian foamy virus, and foamy virus)	5.39E-8	2.17E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	53
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Ape foamy virus (nested in Old World monkey and ape foamy virus, simian foamy virus, and foamy virus)	2.01E-8	8.30E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	52
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Ape foamy virus (nested in Old World monkey and ape foamy virus, simian foamy virus, and foamy virus)	7.48E-8	9.6E5	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	66
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Fereuungulata foamy virus (nested in foamy virus)	5.8E-9	88.7E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	750

Group VI/RT-RNA virus	Retroviridae	Spumavirus	Foamy virus	5.6E-9	98.9E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	250
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Old World monkey and ape foamy virus (nested in simian foamy virus, and foamy virus)	1.70E-8	27.5E6	Pol coding region	Internal-node calibration under the maximum-likelihood phylogenetic framework	(129)	120
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Old World monkey and ape foamy virus (nested in simian foamy virus, and foamy virus)	8.1E-9	31.56E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	123
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Old World monkey foamy virus (nested in Old World monkey and ape foamy virus, simian foamy virus, and foamy virus)	1.27E-8	11.50E6	Pol coding region	Dividing the Bayesian posterior distribution of nucleotide substitution estimate by the distribution of the timescale of evolution, inferred under the viral-host co-speciation assumption	(128)	225
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Simian foamy virus (nested in foamy virus)	7.79E-9	43E6	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(130)	145
Group VI/RT-RNA virus	Retroviridae	Spumavirus	Simian foamy virus (nested in foamy virus)	2.14E-8	43.47E6	Pol coding region	Internal-node calibration under the Bayesian phylogenetic framework	(131)	137
Group VII/RT-DNA virus	Hepadnaviridae	Avihepadnavirus	Avian hepatitis B virus	2.15E-8	19E6	Pol coding region	Dividing a maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(132)	467
Group VII/RT-DNA virus	Hepadnaviridae	Avihepadnavirus	Avian hepatitis B virus	6.80E-8	19E6	Pol coding region	Dividing a maximum-likelihood nucleotide substitution estimate by the timescale of evolution, inferred under the viral-host co-speciation assumption	(132)	495
Group VII/RT-DNA virus	Hepadnaviridae	Orthohepadnavirus	Human hepatitis B virus	2.2E-6	6600	S/P region	Internal-node calibration under the Bayesian phylogenetic framework	(133)	38

2 †Values were directly taken from the original study.

3 When several estimates were available but the best-fit value was not indicated, a geometric mean was used.

4 When only the upper- and lower-bound rate estimates were reported, calculated based on the bound of evolutionary timescales, a harmonic mean rate estimate was used.

5 When only the upper- and lower-bound rate estimates were reported, calculated based on the bound of nucleotide substitution estimates, an arithmetic mean rate estimate was used.

6 \*They were not sampled, and used in the TDRP analyses at the level of viral groups due to the sampling constraint criteria; however they were used in the TDRP analyses at the level of viral genera.

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